

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 01:32:29 ; Search time 170.806 Seconds
(without alignments)
822.965 Million cell updates/sec

Title: US-09-856-979-7
Perfect score: 365
Sequence: 1 tcagccagaccatgggggc.....tccatcaagccgcgcgatg 365

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

1: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match | Length | ID | Description |
|------------|-------|-------|--------|--------|---------------------|--------------------|
| 1 | 365 | 100.0 | 5349 | 10 | US-09-970-921-7 | Sequence 7, Appli |
| 2 | 365 | 100.0 | 6539 | 9 | US-09-509-945-5 | Sequence 5, Appli |
| 3 | 365 | 100.0 | 6548 | 9 | US-09-509-945-4 | Sequence 4, Appli |
| 4 | 35 | 9.6 | 1241 | 12 | US-10-044-090-274 | Sequence 274, App |
| 5 | 31.6 | 8.7 | 918 | 10 | US-09-815-242-9784 | Sequence 9784, Ap |
| 6 | 31.2 | 8.5 | 385 | 10 | US-09-783-590-6496 | Sequence 6496, Ap |
| 7 | 31 | 8.5 | 587 | 10 | US-09-878-574-4548 | Sequence 4548, Ap |
| 8 | 30.6 | 8.4 | 300 | 10 | US-09-294-0938-3715 | Sequence 3715, Ap |
| 9 | 30.6 | 8.4 | 436 | 10 | US-09-728-445-698 | Sequence 698, App |
| 10 | 30.6 | 8.4 | 1623 | 9 | US-09-712-363-23 | Sequence 23, Appli |
| 11 | 30.6 | 8.4 | 2073 | 9 | US-10-068-059-7 | Sequence 9, Appli |
| 12 | 30.6 | 8.4 | 2130 | 9 | US-10-068-059-7 | Sequence 9, Appli |
| 13 | 30.6 | 8.4 | 2175 | 9 | US-10-068-059-11 | Sequence 11, Appli |
| 14 | 30.6 | 8.4 | 2241 | 9 | US-10-068-059-5 | Sequence 5, Appli |
| 15 | 30.4 | 8.3 | 3466 | 10 | US-09-938-405-1 | Sequence 1, Appli |
| 16 | 30.2 | 8.3 | 264 | 10 | US-09-923-876-4605 | Sequence 4605, Ap |
| 17 | 30.2 | 8.3 | 155074 | 9 | US-10-036-188-6 | Sequence 6, Appli |
| 18 | 30 | 8.2 | 4450 | 10 | US-09-764-887-497 | Sequence 497, App |
| 19 | 30 | 8.2 | 4454 | 10 | US-09-764-887-496 | Sequence 496, App |

Sequence 3, Appli
Sequence 11, Appli
Sequence 2168, Ap
Sequence 1890, Ap
Sequence 7, Appli
Sequence 29, Appli
Sequence 5, Appli
Sequence 14392, A
Sequence 2300, Ap
Sequence 127, App
Sequence 377, App
Sequence 2, Appli
Sequence 895, App
Sequence 5627, Ap
Sequence 20699, A
Sequence 104, App
Sequence 3, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 455, App
Sequence 20241, A
Sequence 3471, Ap
Sequence 32286, A
Sequence 15780, A
Sequence 41, Appli
Sequence 41, Appli

US-09-970-921-7
Sequence 7, Application US/09970921
Patent No. US20020133845A1
GENERAL INFORMATION:
APPLICANT: Frank Michiels et al.
TITLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2428-0108p
CURRENT APPLICATION NUMBER: US/09/970,921
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 5349
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: other nucleic
OTHER INFORMATION: acid, "T-DNA of pTTS243"
NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: label = RB, "T-DNA right border"
NAME/KEY: misc_feature
LOCATION: Complement((98)..(331))
OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated
OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
NAME/KEY: misc_feature
LOCATION: Complement((332)..(883))
OTHER INFORMATION: label = bar, "region coding for phosphinthrincin
OTHER INFORMATION: acetyl transferase"
NAME/KEY: misc_feature
LOCATION: Complement((884)..(2258))
OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
OTHER INFORMATION: Virus"
NAME/KEY: misc_feature
LOCATION: (2281)..(3969)
OTHER INFORMATION: label = pE1, "promoter of E1 gene of rice (WO
OTHER INFORMATION: 92/13956)"
NAME/KEY: misc_feature
LOCATION: (3970)..(4245)
OTHER INFORMATION: label = synb*, "Improved barstar DNA"
NAME/KEY: misc_feature

ALIGNMENTS

RESULT 1

US-09-970-921-7
Sequence 7, Application US/09970921
Patent No. US20020133845A1
GENERAL INFORMATION:
APPLICANT: Frank Michiels et al.
TITLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2428-0108p
CURRENT APPLICATION NUMBER: US/09/970,921
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 5349
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: other nucleic
OTHER INFORMATION: acid, "T-DNA of pTTS243"
NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORMATION: label = RB, "T-DNA right border"
NAME/KEY: misc_feature
LOCATION: Complement((98)..(331))
OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated
OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
NAME/KEY: misc_feature
LOCATION: Complement((332)..(883))
OTHER INFORMATION: label = bar, "region coding for phosphinthrincin
OTHER INFORMATION: acetyl transferase"
NAME/KEY: misc_feature
LOCATION: Complement((884)..(2258))
OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
OTHER INFORMATION: Virus"
NAME/KEY: misc_feature
LOCATION: (2281)..(3969)
OTHER INFORMATION: label = pE1, "promoter of E1 gene of rice (WO
OTHER INFORMATION: 92/13956)"
NAME/KEY: misc_feature
LOCATION: (3970)..(4245)
OTHER INFORMATION: label = synb*, "Improved barstar DNA"
NAME/KEY: misc_feature

; LOCATION: (4246)..(4577)
; OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
; OTHER INFORMATION: end of chalcone synthase gene"
; NAME/KEY: misc_feature
; LOCATION: Complement((5325)..(5349))
; OTHER INFORMATION: label = LB, "J-DNA left border"
US-09-970-921-7

Query Match 100.0%; Score 365; DB 10; Length 5349;
Best Local Similarity 100.0%; Pred. No. 7.2e-117;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGGCAAAATTTACTACTATTGGCCATACATTAAACACGCTAAAAG 60
DB 3608 TCAGCCAGACCAATGGGGGCAAAATTTACTACTATTGGCCATACATTAAACACGCTAAAAG 3667
QY 61 TCCTACACTCAACCTAACTGTTGAACGGTCCTGTTGGCCCAACGGTGAGATGCAACCTA 120
DB 3668 TCCTACACTCAACCTAACTGTTGAACGGTCCTGTTGGCCCAACGGTGAGATGCAACCTA 3727
QY 121 ATGGACGGGACAACACTCTTTTACCCTGCTACTGCTACATCTGTAGACGGTGGACGCG 180
DB 3728 ATGGACGGGACAACACTCTTTTACCCTGCTACTGCTACATCTGTAGACGGTGGACGCG 3787
QY 181 TGAGTGCTTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 240
DB 3788 TGAGTGCTTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 3847
QY 241 TGACTCACTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 300
DB 3848 TGACTCACTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 3907
QY 301 CCGGCCACGATAACCCATCTAGCATCCCGGCTGCCAGCAAGAGATCCATCAAGCGCTCG 360
DB 3908 CCGGCCACGATAACCCATCTAGCATCCCGGCTGCCAGCAAGAGATCCATCAAGCGCTCG 3967
QY 361 CGATG 365
DB 3968 CGATG 3972

RESULT 2
US-09-509-945-5/c
; Sequence 5, Application US/09509945
; Patent No. US20020166140A1
; GENERAL INFORMATION:
; APPLICANT: HAMADA, Kazuyuki et al.
; TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID GENE
; FILE REFERENCE: 0230-0148P
; CURRENT APPLICATION NUMBER: US/09/509,945
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 6539
; TYPE: DNA
; ORGANISM: Escherichia coli LE392
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Clone: pTS431
US-09-509-945-5

Query Match 100.0%; Score 365; DB 9; Length 6539;
Best Local Similarity 100.0%; Pred. No. 8e-117;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGGCAAAATTTACTACTATTGGCCATACATTAAACACGCTAAAAG 60
DB 2977 TCAGCCAGACCAATGGGGGCAAAATTTACTACTATTGGCCATACATTAAACACGCTAAAAG 2918
QY 61 TCCTACACTCAACCTAACTGTTGAACGGTCCTGTTGGCCCAACGGTGAGATGCAACCTA 120
DB 2917 TCCTACACTCAACCTAACTGTTGAACGGTCCTGTTGGCCCAACGGTGAGATGCAACCTA 2858

QY 121 ATGGACGGGACAACACTCTTTTACCCTGCTACTGCTACATCTCTGTAGACGGTGGACGCG 180
DB 2857 ATGGACGGGACAACACTCTTTTACCCTGCTACTGCTACATCTCTGTAGACGGTGGACGCG 2798
QY 181 TGAGTGCTTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 240
DB 2797 TGAGTGCTTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 2738
QY 241 TGACTCACTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 300
DB 2737 TGACTCACTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 2678
QY 301 CCGGCCACGATAACCCATCTAGCATCCCGGCTGCCAGCAAGAGATCCATCAAGCGCTCG 360
DB 2677 CCGGCCACGATAACCCATCTAGCATCCCGGCTGCCAGCAAGAGATCCATCAAGCGCTCG 2618
QY 361 CGATG 365
DB 2617 CGATG 2613

RESULT 3
US-09-509-945-4/c
; Sequence 4, Application US/09509945
; Patent No. US20020166140A1
; GENERAL INFORMATION:
; APPLICANT: HAMADA, Kazuyuki et al.
; TITLE OF INVENTION: MUTANT BARNASE GENE AND TRANSGENIC PLANT TRANSFORMED BY SAID G
; FILE REFERENCE: 0230-0148P
; CURRENT APPLICATION NUMBER: US/09/509,945
; CURRENT FILING DATE: 2001-04-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 6548
; TYPE: DNA
; ORGANISM: Escherichia coli LE392
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Clone: pTS172
US-09-509-945-4

Query Match 100.0%; Score 365; DB 9; Length 6548;
Best Local Similarity 100.0%; Pred. No. 8e-117;
Matches 365; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAGCCAGACCAATGGGGGCAAAATTTACTACTATTGGCCATACATTAAACACGCTAAAAG 60
DB 2986 TCAGCCAGACCAATGGGGGCAAAATTTACTACTATTGGCCATACATTAAACACGCTAAAAG 2927
QY 61 TCCTACACTCAACCTAACTGTTGAACGGTCCTGTTGGCCCAACGGTGAGATGCAACCTA 120
DB 2926 TCCTACACTCAACCTAACTGTTGAACGGTCCTGTTGGCCCAACGGTGAGATGCAACCTA 2867
QY 121 ATGGACGGGACAACACTCTTTTACCCTGCTACTGCTACATCTCTGTAGACGGTGGACGCG 180
DB 2866 ATGGACGGGACAACACTCTTTTACCCTGCTACTGCTACATCTCTGTAGACGGTGGACGCG 2807
QY 181 TGAGTGCTTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 240
DB 2806 TGAGTGCTTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 2747
QY 241 TGACTCACTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 300
DB 2746 TGACTCACTTGGCCATGACCGTCCTTGGTGTGTCAGTCACCTTGGCCACGCTTGCACCG 2687
QY 301 CCGGCCACGATAACCCATCTAGCATCCCGGCTGCCAGCAAGAGATCCATCAAGCGCTCG 360
DB 2686 CCGGCCACGATAACCCATCTAGCATCCCGGCTGCCAGCAAGAGATCCATCAAGCGCTCG 2627
QY 361 CGATG 365
DB 2617 CGATG 2613


```

: NAME/KEY: misc feature
: LOCATION: (373)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (375)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (384)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-6496

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Query Match 8.5%; Score 31.2; DB 10; Length 385;
Best Local Similarity 47.4%; Pred. No. 0.33;
Matches 90; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

[illegible]

RESULT 7

US-09-878-574-4548/c
; Sequence 4548, Application US/09878574
; Patent No. US20020110548A1

```

1004011
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 454B
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(587)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3028-033-Q1-B1-A2
US-09-878-574-454B

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Query Match 8.5%; Score 31; DB 10; Length 587;

Best Local Similarity 54.5%;
Matches 61; Conservative
0; Mismatches 51; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 225 | GGCGACGCTTGGACCGTGACTACCTGCGACATTTGCCCGCGCGCGTCCCGGGGCGCTTACAA | 284 |
| | | | |
| Db | 586 | GGGACACCTTTGAACCGCCACCCCGCTTCCTCCCTTCACACACTGCATCCGACCCACCT | 527 |
| QY | 285 | AAGCCACACACGACGCGCGGCGACGATACCCATCTAGCATCCCGGTGTC | 336 |
| Db | 526 | AAATTTTCANCGGAACCCCTTCAACCCCGCCAGCTCCGACGCTTCCCGCGCCCGC | 475 |

RESULT 8

```

US-09-294-093B-3715
: Sequence 3715, Application US/09294093B
: Patent No. US20010051335A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Lalgudi, Raghunath, V.
:
: APPLICANT: Ito, Laura, Y.
:
: APPLICANT: Sherman, Bradley, K.
:
: TITLE OF INVENTION: POLYNUCLEOTIDES AND P
:
: FILE REFERENCE: PL-0009 US
:
: CURRENT APPLICATION NUMBER: US/09/294,093B
:
: CURRENT FILING DATE: 1999-04-16
:
: PRIOR APPLICATION NUMBER: 60/082,567
:
: PRIOR FILING DATE: April 21, 1998
:
: NUMBER OF SEQ ID NOS: 6207
:
: SOFTWARE: PERL Program
:
: SEQ ID NO 3715
:
: LENGTH: 300
:
: TYPE: DNA
:
: ORGANISM: Zea mays
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: OTHER INFORMATION: Incyte ID No. US200100
:
: US-09-294-093B-3715

```

Query Match 8.4%; Score 30.6; DB 10; Length 300;
Best Local Similarity 55.0%; Pred. NO. 0.47;
Matches 60; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 175 | GACGCGTGAGGTGCCTTTCCGCATGACCGTCCTTGGTTGTTGCCAGTCACATTGCCGACGCTT | 234 |
| | | - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - | |
| Db | 55 | GCGCGCTCAGGAGGGTTTCGGCGTAGTCTTCTCGCGTGATGCAGCCTCATTAATGCTGGCG | 114 |

235 GCACCGTGACATCACCTGGCACATTTGCCCCCGCCGCGCGCTACA 283

| | | | |
|----|-----|--|-----|
| QY | 235 | GCACCGGTGACTCACCTGCCACATTCGCCCGCGCGCGCGCGCGCGCTACA | 283 |
| | | | |
| Db | 115 | GCAGCGCTCTGGCGCGCGCGCGCGGTGGACGACGACGGCGTCGGTGGTGACA | 163 |

RESULT 9

```

US-09-728-445-698
; Sequence 698, Application US/09728445
; Patent No. US20020102543A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: NO. US20020102543A1el Mutated Mammalian Cells and
; TITLE OF INVENTION: Animals
; FILE REFERENCE: LEX-0102-USA
; CURRENT APPLICATION NUMBER: US/09/728,445
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 698
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-728-445-698

```

Query Match

| | | | | | |
|-----------------------|--------|--------------|--------|------------|------|
| Self match | 8.48; | Score | 25.10; | Length | 450; |
| Best Local Similarity | 65.28; | Pred. No. | 0.57; | | |
| Matches | 45; | Conservative | 0; | Mismatches | 24; |
| | | | | Indels | 0; |
| | | | | Gaps | 0; |

[illegible]

309 GATAACCA 317

Db 182 CCTCCCCCA 190

```
RESULT 10
US-09-712-363-23/c
; Sequence 23, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-23

Query Match      8.4%; Score 30.6; DB 9; Length 1623;
Best Local Similarity 58.1%; Pred. No. 1.1;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGACGCTTGACCGGTGACTACCTGCCACATTGCCCGCGGTGCGCGGCCCTAC 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1313 TTGGCGCGCGTGCCTCGCTCGGCTTCGAGCTTCAGGTCGTCAGGTCGGGCGCGCTTGC 1254

QY 283 AAAAGCCACACAGCGACGCGCGGCCACGATAACC 315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1253 AACAGCGTCACACCCCGCCACCGCGGACGATGCC 1221

RESULT 11
US-10-068-059-9/c
; Sequence 9, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

Query Match      8.4%; Score 30.6; DB 9; Length 1623;
Best Local Similarity 58.1%; Pred. No. 1.1;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGACGCTTGACCGGTGACTACCTGCCACATTGCCCGCGGTGCGCGGCCCTAC 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1313 TTGGCGCGCGTGCCTCGCTCGGCTTCGAGCTTCAGGTCGTCAGGTCGGGCGCGCTTGC 1254

QY 283 AAAAGCCACACAGCGACGCGCGGCCACGATAACC 315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1253 AACAGCGTCACACCCCGCCACCGCGGACGATGCC 1221

RESULT 12
US-10-068-059-7/c
; Sequence 7, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

Query Match      8.4%; Score 30.6; DB 9; Length 2130;
Best Local Similarity 58.1%; Pred. No. 1.3;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGACGCTTGACCGGTGACTACCTGCCACATTGCCCGCGGTGCGCGGCCCTAC 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1820 TTGGCGCGCGTGCCTCGCTCGGCTTCGAGCTTCAGCTCGTCAGGTCGGGCGCGCTTGC 1761

QY 283 AAAAGCCACACAGCGACGCGCGGCCACGATAACC 315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1760 AACAGCGTCACACCCCGCCACCGCGGACGATGCC 1728

RESULT 13
US-10-068-059-11/c
; Sequence 11, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (1)...(2070)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-9

Query Match      8.4%; Score 30.6; DB 9; Length 2073;
Best Local Similarity 58.1%; Pred. No. 1.3;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGACGCTTGACCGGTGACTACCTGCCACATTGCCCGCGGTGCGCGGCCCTAC 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1763 TTGGCGCGCGTGCCTCGCTCGGCTTCGAGCTTCAGCTCGTCAGGTCGGGCGCGCTTGC 1704

QY 283 AAAAGCCACACAGCGACGCGCGGCCACGATAACC 315
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DB 1703 AACAGCGTCACACCCCGCCACCGCGGACGATGCC 1671

RESULT 12
US-10-068-059-7/c
; Sequence 7, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

Query Match      8.4%; Score 30.6; DB 9; Length 2130;
Best Local Similarity 58.1%; Pred. No. 1.3;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGACGCTTGACCGGTGACTACCTGCCACATTGCCCGCGGTGCGCGGCCCTAC 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1820 TTGGCGCGCGTGCCTCGCTCGGCTTCGAGCTTCAGCTCGTCAGGTCGGGCGCGCTTGC 1761

QY 283 AAAAGCCACACAGCGACGCGCGGCCACGATAACC 315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1760 AACAGCGTCACACCCCGCCACCGCGGACGATGCC 1728

RESULT 13
US-10-068-059-11/c
; Sequence 11, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; SEQ ID NO 11
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2172)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-11

Query Match      8.4%; Score 30.6; DB 9; Length 2175;
Best Local Similarity 58.1%; Pred. No. 1.3;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGCAGCTTGCACGCTGACTCAGCTGCACATTCGCCCGCGGTGCGCGCGCCTAC 282
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Db 1865 TTGGCGCGGTGCGCTGCTGCCTTCAGAGTTTCAGTCTGTCAGGGTTCGGGGCGCCTGC 1806

QY 283 AAAAGCCACACACGCGCGCGCCGACGATAACC 315
      || ||| ||||| || ||||| ||||| ||
Db 1805 AACAGCGTCACACACCCACCGCGGACGATGCC 1773

RESULT 14
US-10-068-059-5/c
; Sequence 5, Application US/10068059
; Patent No. US20020155434A1
; GENERAL INFORMATION:
; APPLICANT: Mizzen, Lee A.
; APPLICANT: Hongwei, Liu
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
; FILE REFERENCE: 12071-017002
; CURRENT APPLICATION NUMBER: US/10/068,059
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/266,733
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2238)
; OTHER INFORMATION: Nucleic acids encoding fusion protein
US-10-068-059-5

Query Match      8.4%; Score 30.6; DB 9; Length 2241;
Best Local Similarity 58.1%; Pred. No. 1.4;
Matches 54; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 223 TTGGCGCAGCTTGCACGCTGACTCAGCTGCACATTCGCCCGCGGTGCGCGCGCCTAC 282
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1931 TTGGCGCGGTGCGCTGCTGCCTTCAGCTTCAGTCTGTCAGGGTTCGGGGCGCCTGC 1872

QY 283 AAAAGCCACACACGCGCGCGCCGACGATAACC 315
      || ||| ||||| || ||||| ||||| ||
Db 1871 AACAGCGTCACACACCCACCGCGGACGATGCC 1839

RESULT 15
US-09-938-405-1
; Sequence 1, Application US/09938405
; Patent No. US20020111296A1
; GENERAL INFORMATION:
; APPLICANT: Festoff, Barry W.
; APPLICANT: Morser, Michael J.
; TITLE OF INVENTION: Thrombomodulin Analogs for Use in Recovery of Spinal Cord Injury
; FILE REFERENCE: 51960AUSM1
; CURRENT APPLICATION NUMBER: US/09/938,405
; CURRENT FILING DATE: 2001-08-23
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; PRIOR APPLICATION NUMBER: 60/229,714
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)...(1875)
; OTHER INFORMATION:
; NAME/KEY: mat_peptide
; LOCATION: (205)...()
; OTHER INFORMATION:
US-09-938-405-1

Query Match      8.3%; Score 30.4; DB 10; Length 3466;
Best Local Similarity 63.9%; Pred. No. 2;
Matches 46; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 222 CTGTGGCGACGCTTGCACCGTGACTCAGCTGCACATTCGCCCGCGGTGCGCGCGCCTA 281
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 CCTGTGCCCTCTGTCTCCGCGACGGCCCTGTCCAGTGCCTCCCGCGCTTCCCGCGCCTG 129

QY 282 CAAAAGCCACAC 293
      || ||| ||
Db 130 CACGCGCGCGC 141

Search completed: December 2, 2002, 04:18:35
Job time : 179.806 secs
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